SEARCH:

Title: US-10-590-810-26_COPY_13_555
Perfect score: 2763
Sequence: 1 SPKALEEAPWPPPEGAFVGF..........LAVPLEVEVGIGEDWLSAKE 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 12150526 seqs, 2531973831 residues

Total number of hits satisfying chosen parameters: 12150526

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2763	100.0	543	27	US-09-791-537-91889	Sequence 91889, A
2	2763	100.0	544	39	US-10-917-157-2	Sequence 2, Appli
3	2763	100.0	544	39	US-10-917-157A-2	Sequence 2, Appli
4	2763	100.0	544	39	US-10-917-157B-2	Sequence 2, Appli
5	2763	100.0	545	39	US-10-917-157-4	Sequence 4, Appli
6	2763	100.0	545	39	US-10-917-157A-4	Sequence 4, Appli
7	2763	100.0	545	39	US-10-917-157B-4	Sequence 4, Appli
8	2763	100.0	552	25	US-09-506-153-1	Sequence 1, Appli
9	2763	100.0	552	32	US-10-216-682-1	Sequence 1, Appli
10	2763	100.0	554	1	PCT-US07-78571-3	Sequence 3, Appli
11	2763	100.0	554	12	US-08-202-032A-6	Sequence 6, Appli
12	2763	100.0	554	19	US-08-931-818-6	Sequence 6, Appli
13	2763	100.0	554	38	US-10-850-816-2	Sequence 2, Appli
14	2763	100.0	554	52	US-12-254-969B-6	Sequence 6, Appli
15	2763	100.0	554	53	US-12-330-201A-2	Sequence 2, Appli
16	2763	100.0	554	54	US-12-441-521A-3	Sequence 3, Appli
17	2763	100.0	558	39	US-10-917-157-5	Sequence 5, Appli
18	2763	100.0	558	39	US-10-917-157A-5	Sequence 5, Appli
19	2763	100.0	558	39	US-10-917-157B-5	Sequence 5, Appli
20	2763	100.0	562	25	US-09-506-153-7	Sequence 7, Appli
21	2763	100.0	562	32	US-10-216-682-7	Sequence 7, Appli
22	2763	100.0	562	35	US-10-590-810-26	Sequence 26, Appl
23	2763	100.0	605	43	US-11-327-195-44	Sequence 44, Appl
24	2763	100.0	605	43	US-11-327-195A-44	Sequence 44, Appl
25	2763	100.0	605	43	US-11-327-195B-44	Sequence 44, Appl

26	2763	100.0	605	43	US-11-327-845-43	Sequence 43, Appl
27	2763	100.0	606	43	US-11-327-195-41	Sequence 41, Appl
28	2763	100.0	606	43	US-11-327-195A-41	Sequence 41, Appl
29	2763	100.0	606	43	US-11-327-195B-41	Sequence 41, Appl
30	2763	100.0	606	43	US-11-327-845-40	Sequence 40, Appl
31	2763	100.0	625	43	US-11-327-195-43	Sequence 43, Appl
32	2763	100.0	625	43	US-11-327-195A-43	Sequence 43, Appl
33	2763	100.0	625	43	US-11-327-195B-43	Sequence 43, Appl
34	2763	100.0	625	43	US-11-327-845-42	Sequence 42, Appl
35	2763	100.0	626	43	US-11-327-195-40	Sequence 40, Appl
36	2763	100.0	626	43	US-11-327-195A-40	Sequence 40, Appl
37	2763	100.0	626	43	US-11-327-195B-40	Sequence 40, Appl
38	2763	100.0	626	43	US-11-327-845-39	Sequence 39, Appl
39	2763	100.0	632	1	PCT-US03-32954-4	Sequence 4, Appli
40	2763	100.0	632	1	PCT-US03-32954-6	Sequence 6, Appli
41	2763	100.0	632	1	PCT-US03-32954-8	Sequence 8, Appli
42	2763	100.0	632	32	US-10-256-705-4	Sequence 4, Appli
43	2763	100.0	632	32	US-10-280-139-4	Sequence 4, Appli
44	2763	100.0	632	32	US-10-280-139-6	Sequence 6, Appli
45	2763	100.0	632	32	US-10-280-139-8	Sequence 8, Appli

ALIGNMENTS

```
RESULT 1
US-09-791-537-91889
; Sequence 91889, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
MEMBERS AND
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91889
;   LENGTH: 543
;   TYPE: PRT
;   ORGANISM: pdb 1KTQ
US-09-791-537-91889

  Query Match             100.0%;  Score 2763;  DB 27;  Length 543;
  Best Local Similarity   100.0%;
  Matches  543;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEAR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEAR 60

Qy         61 GLLAKDLSVLALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLLAKDLSVLALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALS 120
```

```
Qy         121 ERLFANLWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIAR 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ERLFANLWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIAR 180

Qy         181 LEAEVFRLAGHPFNLNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIV 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 LEAEVFRLAGHPFNLNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIV 240

Qy         241 EKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 EKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP 300

Qy         301 LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGV 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGV 360

Qy         361 PREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEK 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 PREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEK 420

Qy         421 TLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLF 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLF 480

Qy         481 PRLEEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLS 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 PRLEEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLS 540

Qy         541 AKE 543
               |||
Db         541 AKE 543
```

21
1688
DNA
Thermus aquaticus

CDS
(3)..(1688)

21

```
cc atg gcc tct ggt ggc ggt ggc tgt ggt ggc ggt ggc agc ccc aag        47
   Met Ala Ser Gly Gly Gly Gly Cys Gly Gly Gly Gly Ser Pro Lys
   1               5                   10                  15
gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa ggg gcc ttc gtg ggc        95
Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly
                20                  25                  30
ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc gat ctt ctg gcc ctg       143
Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu
            35                  40                  45
gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc ccc gag cct tat aaa       191
Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys
        50                  55                  60
gcc ctc agg gac ctg aag gag gcg cgg ggg ctt ctc gcc aaa gac ctg       239
Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu
    65                  70                  75
agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc ccg ccc ggc gac gac       287
```

```
Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp
80                  85                  90                  95
ccc atg ctc ctc gcc tac ctc ctg gac cct tcc aac acc acc ccc gag      335
Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu
                100                 105                 110
ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg gag gag gcg ggg gag      383
Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu
            115                 120                 125
cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac ctg tgg ggg agg ctt      431
Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu
        130                 135                 140
gag ggg gag gag agg ctc ctt tgg ctt tac cgg gag gtg gag agg ccc      479
Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro
    145                 150                 155
ctt tcc gct gtc ctg gcc cac atg gag gcc acg ggg gtg cgc ctg gac      527
Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp
160                 165                 170                 175
gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg gcc gag gag atc gcc      575
Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala
                180                 185                 190
cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc cac ccc ttc aac ctc      623
Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu
            195                 200                 205
aac tcc cgg gac cag ctg gaa agg gtc ctc ttt gac gag cta ggg ctt      671
Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu
        210                 215                 220
ccc gcc atc ggc aag acg gag aag acc ggc aag cgc tcc acc agc gcc      719
Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala
    225                 230                 235
gcc gtc ctg ggg gcc ctc cgc gag gcc cac ccc atc gtg gag aag atc      767
Ala Val Leu Gly Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile
240                 245                 250                 255
ctg cag tac cgg gag ctc acc aag ctg aag agc acc tac att gac ccc      815
Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro
                260                 265                 270
ttg ccg gac ctc atc cac ccc agg acg ggc cgc ctc cac acc cgc ttc      863
Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe
            275                 280                 285
aac cag acg gcc acg gcc acg ggc agg cta agt agc tcc gat ccc aac      911
Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn
        290                 295                 300
ctc cag aac atc ccc gtc cgc acc ccg ctt ggg cag agg atc cgc cgg      959
Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg
    305                 310                 315
gcc ttc atc gcc gag gag ggg tgg cta ttg gtg acc ctg gac tat agc     1007
Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Thr Leu Asp Tyr Ser
320                 325                 330                 335
cag ata gag ctc agg gtg ctg gcc cac ctc tcc ggc gac gag aac ctg     1055
Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu
                340                 345                 350
atc cgg gtc ttc cag gag ggg cgg gac atc cac acg gag acc gcc agc     1103
Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser
            355                 360                 365
tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac ccc ctg atg cgc cgg     1151
Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg
        370                 375                 380
gcg gcc aag acc atc aac ttc ggg gtc ctc tac ggc atg tcg gcc cac     1199
Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His
    385                 390                 395
cgc ctc tcc cag gag cta gcc atc cct tac gag gag gcc cag gcc ttc     1247
Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe
400                 405                 410                 415
att gag cgc tac ttt cag agc ttc ccc aag gtg cgg gcc tgg att gag     1295
```

```
Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu
                420                 425                 430
aag acc ctg gag gag ggc agg agg cgg ggg tac gtg gag acc ctc ttc     1343
Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe
            435                 440                 445
ggc cgc cgc cgc tac gtg cca gac cta gag gcc cgg gtg aag agc gtg     1391
Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val
        450                 455                 460
cgg gag gcg gcc gag cgc atg gcc ttc aac atg ccc gtc cag ggc acc     1439
Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr
    465                 470                 475
gcc gcc gac ctc atg aag ctg gct atg gtg aag ctc ttc ccc agg ctg     1487
Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu
480                 485                 490                 495
gag gaa atg ggg gcc agg atg ctc ctt cag gtc cac gac gag ctg gtc     1535
Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val
                500                 505                 510
ctc gag gcc cca aaa gag ggg gcg gag gcc gtg gcc cgg ctg gcc aag     1583
Leu Glu Ala Pro Lys Glu Gly Ala Glu Ala Val Ala Arg Leu Ala Lys
            515                 520                 525
gag gtc atg gag ggg gtg tat ccc ctg gcc gtg ccc ctg gag gtg gag     1631
Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu
        530                 535                 540
gtg ggg ata ggg gag gac agg ctc tcc gcc aag gag gcg gcc gca ctg     1679
Val Gly Ile Gly Glu Asp Arg Leu Ser Ala Lys Glu Ala Ala Ala Leu
    545                 550                 555
gtg ccg cgc                                                         1688
Val Pro Arg
560
```

W550 tryptophan

SEQ ID NO:26 is Thermus aquaticus

EAST SEARCH:

US 7488816 11/065,943 (Wilder exmnr)

```
IS&R    L1      1       ("7417133").PN.US-PGPUB; USPAT; USOCR 2010/07/12 10:22
BRS     L3      16      W550    USPAT   2010/07/12 10:31
BRS     L4      62051   polymerase      USPAT   2010/07/12 10:35
BRS     L5      17552   l4 and tryptophan       USPAT   2010/07/12 10:35
BRS     L6      561     l4 and tryptophan.clm. USPAT   2010/07/12 10:36
BRS     L7      4440    "550".clm.      USPAT   2010/07/12 10:56
BRS     L8      108     l4 and l7       USPAT   2010/07/12 10:57
```

d his

```
          (FILE 'HOME' ENTERED AT 11:32:56 ON 12 JUL 2010)

     FILE 'MEDLINE, CAPLUS, BIOSIS, BIOTECHNO, EMBASE, JAPIO' ENTERED AT
     11:36:07 ON 12 JUL 2010
L1       1642496 S POLYMERASE
L2             0 S L1 AND W550
L3          4979 S L1 AND TRYPTOPHAN
L4             3 S L3 AND 550
```

```
L5          1522 S L1 AND 550
L6          2207 S L3 AND (MUTA? OR VARIAN? OR SUBSTIT?)
L7            12 S L6 AND TAQ
L8             8 DUP REM L7 (4 DUPLICATES REMOVED)

     FILE 'MEDLINE, BIOSIS, CAPLUS, BIOTECHNO, EMBASE, JAPIO' ENTERED AT
     13:52:04 ON 12 JUL 2010
L9       1642496 S POLYMERASE
L10          245 S L9 AND 827
L11            0 S L10 AND TRYPTOPHAN
L12            2 S L10 AND TAQ
```

L8   ANSWER 4 OF 8 CAPLUS

AN   2004:171780 CAPLUS

DN   140:351362

TI   A novel strategy to engineer DNA polymerases for enhanced processivity and improved performance in vitro

AU   Wang, Yan; Prosen, Dennis E.; Mei, Li; Sullivan, John C.; Finney, Michael; Vander Horn, Peter B.

CS   Department of Research and Development, MJ Bioworks Inc., South San Francisco, CA, 94080, USA

SO   Nucleic Acids Research (2004), 32(3), 1197-1207
     CODEN: NARHAD; ISSN: 0305-1048

PB   Oxford University Press

DT   Journal

LA   English

AB   Mechanisms that allow replicative DNA polymerases to attain high processivity are often specific to a given polymerase and cannot be generalized to others. Here the authors report a protein engineering-based approach to significantly improve the processivity of DNA polymerases by covalently linking the polymerase domain to a sequence non-specific dsDNA binding protein. Using Sso7d from Sulfolobus solfataricus as the DNA binding protein, the authors demonstrate that the processivity of both family A and family B polymerases can be significantly enhanced. By introducing point mutations in Sso7d, the authors show that the dsDNA binding property of Sso7d is essential for the enhancement. The authors present evidence supporting two novel conclusions. First, the fusion of a heterologous dsDNA binding protein to a polymerase can increase processivity without compromising catalytic activity and enzyme stability. Second, polymerase processivity is limiting for the efficiency of PCR, such that the fusion enzymes exhibit profound advantages over unmodified enzymes in PCR applications. This technol. has the potential to broadly improve the performance of nucleic acid modifying enzymes.